

SEQUENCE LISTING

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<120> SORBITOL DEHYDROGENASE, GENE ENCODING THE SAME AND USE THEREOF

<130> 213930US0PCT

<140> 09/926,163 <141> 2001-09-17

<150> PCT/JP00/01608

<151> 2000-03-16

<150> JP11/72810

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<151> 1999-08-06

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| catgecegge ettgteggte | codatcaaca acc | raaccaa aa | accacacaa aatto | c atq 539 |
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| catgeodye cttytogyto | codgecageg acc | .ggcccga aa | iccaeggag aaree | Met 1 |
| att acg cgc gaa acc c Ile Thr Arg Glu Thr L 5 | tt aag tct ctt eu Lys Ser Leu 10 | cct gcc aa Pro Ala As | at gtc cag gct sn Val Gln Ala 15 | ccc 587 Pro |
| ccc tat gac atc gac g Pro Tyr Asp Ile Asp G 20 | gg atc aag cct ly Ile Lys Pro 25 | ggg atc gt Gly Ile Va | tg cat ttc ggt al His Phe Gly 30 | gta 635 Val |
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| gaa cac gct ccg gac t Glu His Ala Pro Asp T 50 5 | gg gcg att gtt rp Ala Ile Val 5 | ggt gtt gg Gly Val Gl 60 | gc ctg acg ggc ly Leu Thr Gly | agt 731 Ser 65 |
| gac cgt tca aag aaa a Asp Arg Ser Lys Lys L 70 | aa gcc gag gaa ys Ala Glu Glu | ttc aag go Phe Lys Al 75 | cc cag gac tgc la Gln Asp Cys 80 | ctg 779 Leu |
| tat tcc ctg acc gag a Tyr Ser Leu Thr Glu T 85 | cg gct ccg tcc hr Ala Pro Ser 90 | ggc aag ag | gc acg gtg cgc er Thr Val Arg 95 | gtc 827 Val |
| atg ggc gcg ctg cgt g Met Gly Ala Leu Arg A 100 | ac tat ctg ctt sp Tyr Leu Leu 105 | gdc ccg gd | cc gat ccg gaa la Asp Pro Glu 110 | gcc 875 Ala |
| gtg ctg aag cat ctt g Val Leu Lys His Leu V 115 | | Ile Arg I | | |
| atc acg gaa ggc ggc t Ile Thr Glu Gly Gly T 130 | ac aac atc aac Yr Asn Ile Asn 35 | gag acg ac Glu Thr Tl | cc ggt gcg ttc hr Gly Ala Phe | gat 971 Asp 145 |
| ctg gag aat gcg gca g Leu Glu Asn Ala Ala V 150 | ta aag gcc gac al Lys Ala Asp | ctc aag aa Leu Lys As 155 | ac ccg gaa aag sn Pro Glu Lys 160 | ccg 1019 Pro |
| tct acc gtt ttc ggt t Ser Thr Val Phe Gly T 165 | ac gtg gtc gag 'yr Val Val Glu 170 | gcc ctg c | gt cgt cgt tgg rg Arg Arg Trp 175 | gat 1067 Asp |
| gcc ggt ggt aag gca t Ala Gly Gly Lys Ala P 180 | tt acg gtc atg The Thr Val Met 185 | tcc tgt ga | at aac ctg cgt sp Asn Leu Arg | cat 1115 His |
| aac ggc aat gtc gcc c Asn Gly Asn Val Ala A 195 | gc aag gcc ttc rg Lys Ala Phe 200 | Leu Gly T | at gcg aag gcg yr Ala Lys Ala 05 | cgc 1163 Arg |

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|-------------------|------------|-------------------|-------------------|------------|-------------------|------------|-------------------|-------------------|-------------|-------------------|------------|-------------------|-------------------|------------|-------------------|---|-------|
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| | | | | | | | | | | tcg Ser | | | | | | | 1259 |
| | | | | | | | | | | gac Asp | | | | | | | 1307 |
| gag Glu | gat Asp | ttc Phe 260 | cat His | cag Gln | tgg Trp | gtg Val | ctg Leu 265 | gaa Glu | gac Asp | cag Gln | ttt Phe | gcg Ala 270 | gat Asp | ggc Gly | cgt Arg | | 1355 |
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| tgg Trp 290 | gag Glu | tac Tyr | gtc Val | aag Lys | atc Ile 295 | cga Arg | atg Met | ctc Leu | aat Asn | gca Ala 300 | Gly 999 | cat His | gtc Val | atg Met | ctc Leu 305 | | 1451 |
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| gag Glu | aag Lys | ggc Gly 420 | Gly 999 | acg Thr | tat Tyr | gaa Glu | tcg Ser 425 | tcc Ser | gag Glu | ccg Pro | act | tat Tyr 430 | ggc Gly | gac Asp | gcc Ala | | 1835 |
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| Glu Trp Lys Leu Ala Lys Ala Asp Asp 435 | Phe Glu Ser Ser Leu Lys Leu 445 | |
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| ccg gcg ttc gat ggg tgg cgc dat ctg Pro Ala Phe Asp Gly Trp Arg Asp Leu 450 455 | gat acg tcc gaa ctg gat caa 1931 Asp Thr Ser Glu Leu Asp Gln 460 465 | L |
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Val Gly Asn Phe Phe Arg Ala His Glu Ala Phe Tyr Val Glu Gln Ile 35 40 45

Leu Glu His Ala Pro Asp Trp Ala Ile Val Gly Val Gly Leu Thr Gly 50 55

Ser Asp Arg Ser Lys Lys Lys Ala Glu Glu Phe Lys Ala Gln Asp Cys
65 70 75 80

Leu Tyr Ser Leu Thr Glu Thr Ala Pro Ser Gly Lys Ser Thr Val Arg

85 \ 90 95

Val Met Gly Ala Leu Arg Asp Tyr Leu Leu Ala Pro Ala Asp Pro Glu 100 105 110

Ala Val Leu Lys His Leu Val Asp Pro Ala Ile Arg Ile Val Ser Met
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Thr Ile Thr Glu Gly Gly Tyr Asn Ile Asn Glu Thr Thr Gly Ala Phe 130 135 140

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Pro Ser Thr Val Phe Gly Tyr Val Val Glu Ala Leu Arg Arg Trp
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Asp Ala Gly Gly Lys Ala Phe Thr Val Met Ser Cys Asp Asn Leu Arg
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His Asn Gly Asn Val Ala Arg Lys Ala Phe Leu Gly Tyr Ala Lys Ala
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Arg Asp Pro Glu Leu Ala Lys Trp Ile Glu Glu Asn Ala Thr Phe Pro 210 220

Asn Gly Met Val Asp Arg Ile Thr Pro Thr Val Ser Ala Glu Ile Ala 225 230 235 240

Lys Lys Leu Asn Ala Ala Ser Gly Leu Asp Asp Asp Leu Pro Leu Val 245 250 255

Ala Glu Asp Phe His Gln Trp Val Leu Glu Asp Gln Phe Ala Asp Gly 260 265 270

Arg Pro Pro Leu Glu Lys Ala Gly Val Gln Met Val Gly Asp Val Thr 275 280 285

Asp Trp Glu Tyr Val Lys Ile Arg Met Leu Asn Ala Gly His Val Met 290 295 300

Leu Cys Phe Pro Gly Ile Leu Val Gly Tyr Glu Asn Val Asp Asp Ala 305 310 315 320

Ile Glu Asp Ser Glu Leu Leu Gly Asn Leu Lys Asn Tyr Leu Asn Lys 325 330 335

Asp Val Ile Pro Thr Leu Lys Ala Pro Ser Gly Met Thr Leu Glu Gly 340 345 350

Tyr Arg Asp Ser Val Ile Ser Arg Phe Ser Asn Lys Ala Met Ser Asp 355 360 365

Gln Thr Leu Arg Ile Ala Ser Asp Gly Cys Ser Lys Val Gln Val Phe 370 380

Trp Thr Glu Thr Val Arg Arg Ala Ile Glu Asp Lys Arg Asp Leu Ser 385 390 400

Arg Ile Ala Phe Gly Ile Ala Ser Tyr Leu Glu Met Leu Arg Gly Arg

Asp Glu Lys Gly Gly Thr Tyr Glu Ser Ser Glu Pro Thr Tyr Gly Asp
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Ala Glu Trp Lys Leu Ala Lys Ala Asp Asp Phe Glu Ser Ser Leu Lys
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440
445

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